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Fragment screening by crystallography –efficient workflow for MX users at BESSY II

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Macromolecular crystallography (MX) can identify compounds like fragments in their 3D structural context of the protein target, in enhanced through-put. At the MX beamlines at BESSY II, a workflow including dedicated tools, efficient compound libraries and convenient software solutions was established and optimized to provide for efficient screening. Developments like the F2X libraries, the EasyAccess Frame, fspipeline and FragMAXapp elevate the user experience and screening efficiency.

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